AMENDMENTS TO THE CLAIMS

1.   (currently amended): A method for reconstructing metabolism of [[an]] a eukaryotic organism in a non-disease state and a disease state, comprising:

      (a)   collecting data regarding the organism's metabolism for said non-disease and disease states;

      (b)   linking the data into metabolic pathways;

      (c)   linking said metabolic pathways to functional information, disease manifestations and/or high-throughput screening information;

      (d)   identifying interconnections between the metabolic pathways; and

      (d)(e)   creating a map maps of the organism's metabolism in said non-disease and disease states by integrating information obtain obtained in steps (a), (b), [[and]] (c) and (d).

2.   (canceled).

3.   (currently amended): A method for identifying a drug target targets comprising:

      (a)   collecting data regarding [[the]] a eukaryotic organism's metabolism for both a non-disease state and a disease state states;

      (b)   linking the data into metabolic pathways;

      (c)   linking said metabolic pathways to functional information, disease manifestations and/or high-throughput screening information;

      (d)   identifying interconnections between the metabolic pathways;

      (d)(e)   creating a map maps of the organism's metabolism in said non-disease and disease states by integrating information obtain obtained in steps (a), (b), [[and]] (c) and (d)[[.]]; and

      (e)(f)   identifying a drug target targets by comparing differences between said non-disease and disease states using the map maps.

4.   (new): The method of claim 1 or 3, wherein said eukaryotic organism is a mammal.

5.   (new): The method of claim 4, wherein said mammal is a human.

6.   (new): The method of claim 1 or 3, wherein said data regarding the organism's metabolism comprises expressed sequence tag data.

7.   (new): The method of claim 1 or 3, wherein said data regarding the organism's metabolism comprises biochemical units comprising metabolic steps, chemical compounds, reactions and/or enzymatic functions.

8.   (new): The method of claim 7, wherein said enzymatic functions comprise genes and proteins.

9.   (new): The method of claim 7, wherein each of said biochemical units is linked to an annotation table, said annotation table comprising at least one field.

10   (new): The method of claim 9, wherein said at least one field is selected from the group consisting of organ localization, tissue localization, intracellular localization, intracellular compartmentalization, subcellular localization in another organism, a relationship to a disease, and a reference to an information source.

11.   (new): The method of claim 1 or 3, wherein at least one of said metabolic pathways comprises a chitinase.

12.   (new): The method of claim 11, wherein said chitinase is HC gp-39.